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SEQUENCE LISTING

<110>. He et al. Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 and 4 <130> PF140 ' US 08/334,251 <140> <141> 1994-11-01 <160> <170> PatentIn version 3.0 <210> <211> <212> DNA Homo sapiens <400> gcacgagaaa ctttgctgtg cgcgttctcc cgcgcgcggg ctcaactttg tagagcgagg ggccaacttg gcagagcgcg cggccagctt tgcagagagc gccctccagg gactatgcgt 120 geggggacac gggtegettt gggetettee acceetgegg agegeactae eeegageeag 180 gggcggtgca agccccgccc ggccctaccc agggcggctc ctccctccgc agcgccgaga 240 cttttagttt cgctttcgct aaaggggccc cagaccettg ctgcggagcg acggagagag 3 0.0 actgtgccag teccageege ectacegeeg tgggaacgat ggcagatgat cagggetgta 360 ttgaagagca gggggttgag gattcagcaa atgaagattc agtggatgct aagccagacc 420 qqtcctcqtt tqtaccqtcc ctcttcagta agaagaagaa aaatgtcacc atgcgatcca 48Ó tcaagaccac ccgggaccga gtgcctacat atcagtacaa catgaatttt gaaaagctgg 540 gcaaatgcat cataataaac aacaagaact ttgataaagt gacaggtatg ggcgttcgaa 600 acggaacaga caaagatgcc gaggcgctct tcaagtgctt ccgaagcctg ggttttgacg 660 tgattgtcta taatgactgc tcttgtgcca agatgcaaga tctgcttaaa aaagcttctg 720 aagaggacca tacaaatgcc gcctgcttcg cctgcatcct.cttaagccat ggagaagaaa 780 atgtaattta tgggaaagat ggtgtcacac caataaagga tttgacagcc cactttaggg 840 gggatagatg caaaaccctt ttagagaaac ccaaactctt cttcattcag gcttgccgag 900 ggaccgaget tgatgatgee atccaggeeg acteggggee cateaatgae acagatgeta 960 atcotogata caagatocca gtggaagotg acttootott cgcctattoc acggttocag 1020 1080 gctattactc gtggaggagc ccaggaagag gctcctggtt tgtgcaagcc ctctgctcca tcctggagga gcacggaaaa gagctggaaa tcatgcaaat cctcaccagg gtgaatgaca 1140 gagttgccag gcactttgag tctcagtctg atgacccaca cttccatgag aagaagcaga 1200

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Ala	Asn	Glu	Asp 20	Ser	Val	Asp	Ala	Lys 25	Pro	Asp	Arg	Ser	Ser 30	Phe	Val		
Pro	Ser	Leu 35	Phe	Ser	Lys	Lys	Lys 40	Lys	Asn	Val	Thr	Met 45	Arg	Ser	Ile		
Lys	Thr 50	Thr	Arg	Asp	Arg	Val 55	Pro	Thr	Tyr	Gln	Tyr 60	Asn	Met	Asn	Phe		و د
Glu 65	Lys	Leu	Gly	Lys	Cys 70	Ile	Ile	Ile	Asn	Asn 75	Lys	Asn	Phe	Asp	Lys 80		
Val	Thr	Gly	Met	Gly 85°	Val	Arg	Asn	Gly	Thr 90	Asp	Lys	Asp	Ala	Glu 95	Ala		
Leu	Phe	Lys	Cys 100	Phe	Arg	Ser	Leu	Gly 105	Phe	Asp	Val	Ile	Val 110	Tyr	Asn		
Asp	Cys	Ser 115	Cys	Ala	Lys	Met	Gln 120	Asp	Leu	Leu	Lys	Lys 125	Ala	Ser	Glu		
Glu	Asp 130	His	Thr	Asn	Ala	Ala 135	Cys	Phe	Ala	Cys	Ile 140	Leu	Leu	Ser	His	: ·	
Gly 145	Glu	Glu	Asn	Val	Ile 150	Tyr	Gly	Lys	Asp	Gly 155	Val	Thr	Pro	Ile	Lys 160		
Asp	Leu	Thr	Ala	His 165	Phe	Arg	Gly		Arg 170	Cys	Lys	Thr	Leu	Leu 175	Glu		· · · · · · · · · · · · · · · · · · ·
Lys	Pro	Lys	Leu 180	Phe	Phe	Ile	Gln	Ala 185	Cys	Arg	Gly	Thr	Glu 190	Leu	Asp		
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Pro	Arg 210	Tyr	Lys	Ile	Pro	Val 215	Glu	Ala	Asp	Phe	Leu 220		Ala	Tyr	Ser		
Thr 225	Val	Pro	Gly	Tyr	Tyr 230	Ser	Trp	Arg	Ser	Pro 235	Gly	Arg	Gly	Ser	Trp 240		

Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Glu Leu Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln <210> 1159 DNA Homo sapiens gcacgagcgg atgggtgcta ttgtgaggcg gttgtagaag agtttcgtga gtgctcgcag 60 ctcatacetg tggctgtgta teegtggeea cagetggttg gegtegeett gaaateeeag 120 gccgtgagga gttagcgagc cctgctcaca ctcggcgctc tggttttcgg tgggtgtgcc 180 ctgcacctgc ctcttcccgc attctcatta ataaaggtat ccatggagaa cactgaaaac 240 tcaqtqqatt caaaatccat taaaaatttq qaaccaaaga tcatacatgg aagcgaatca 300 atggactctg gaatatccct ggacaacagt tataaaatgg attatcctga gatgggttta 360 tgtataataa ttaataataa gaattttcat aaaagcactg gaatgacatc tcggtctggt 420 acagatgteg atgeageaaa eeteagggaa acatteagaa aettgaaata tgaagteagg 480 aataaaaatg atcttacacg tgaagaaatt gtggaattga tgcgtgatgt ttctaaagaa 540 gatcacagca aaaggagcag ttttgtttgt gtgcttctga gccatggtga agaaggaata 600 attittggaa caaatggacc tgttgacctg aaaaaaataa caaactittt cagaggggat 660 cgttgtagaa gtctaactgg aaaacccaaa cttttcatta ttcaggcctg ccgtggtaca 720 gaactggact gtggcattga gacagacagt ggtgttgatg atgacatggc gtgtcataaa 780 ataccagtgg aggeegactt ettgtatgea taeteeacag caectggtta ttattettgg 840 cgaaattcaa aggatggete etggtteate cagtegettt gtgeeatget gaaacagtat 900 gccgacaágc ttgaatttat gcacattctt acccgggtta accgaaaggt ggcaacagaa 960 tttgagtcct tttcctttga cgctactttt catgcaaaga aacagattcc atgtattgtt 1020

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Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile 35 40 45

Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
50 55 60

Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn 65 70 75 80

Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile 85 90 95

Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser 100 105 110

Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe 115 120 125

Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg 130 135 140

Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile 145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser 165 170 175

Gly Val Asp Asp Met Ala Cys His Lys Ile Pro Val Glú Ala Asp 180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn 195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys 210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn 225 230 235 240

Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe 245 250 255

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Leu Tyr Phe Tyr His
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